

Fig. 1.

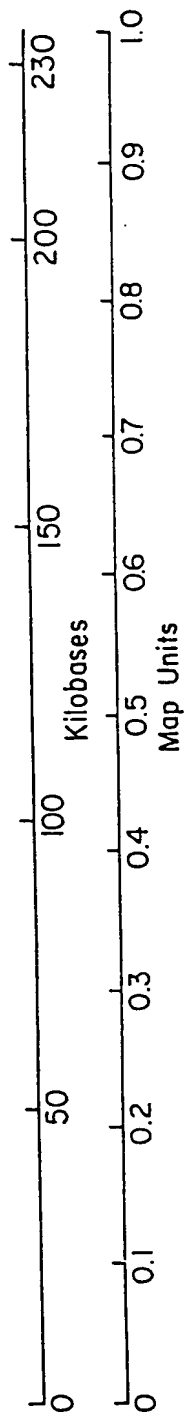
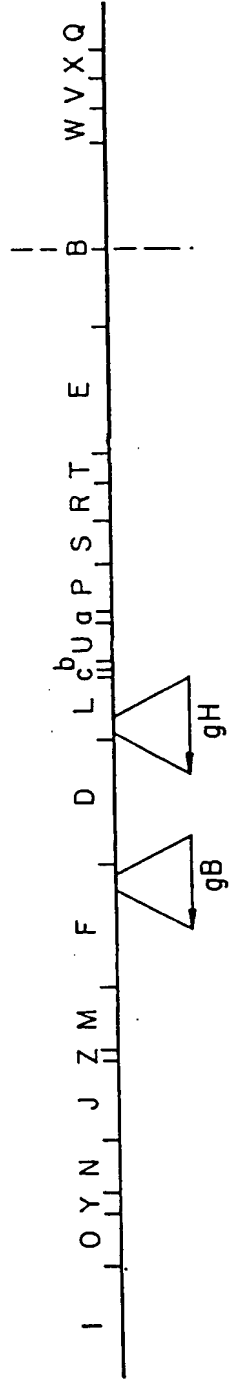


Fig. 2(a)

EDV MTRRR-----VLSVVVLLAALACRLGAUTPEQ-----PAPPATTVOPTATROO--
CMV MESR-----IWCLVVCVNLCIVCLGAAVSSSSTSHATSSTHNGSHTSRITTSAQTRSVMYHQHVITSSEAVSH
HSV MRQGAARGCRWFVVWVALGLTLGLVLVASAAPSSPGTPGVAAAATAQAANGGPATPAPPAPGPAPTGTDTKPKK

EDV -----TSFPFRVCELSHGD LFRFSSDIQCPSF-GTRE
CMV -----RANETIYNTTLKYGVVVGN TTKYPYRVCSMAQGTDLIRFERNI ICTSMKXPINE
SV -----NKYPKNPBPPBPAGDNATVAAGHA TIREFHLRDIKAENTDANFYVCPPPTGATVVOFEOPRRRCPTR--PEGO

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EBV      NHTEGLLMVFKNDIIPYSFKVRSYTKIVTNILINYNGWYADSVTNRHEEKIFSVDSEYET-DQMDTIYQCYN
CMV      DLDEGIMVVYKRNIVAHITFKVRVYOKVLTERRSAYIYYTTYLLGSNTEYVAPPMWEI-HHINKFAQCYS
HSV      NYTEGIAVVFKENIAPYKKFATMYKKDVTVSQVWFHGHRYSQFMGIFEDRAPVPFEVVDKINAKGVCRST
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EBV	VKMTK	DGLTR	YVDR	CGNIT	VNLK	PTG	GLANG	VRRY	ASOT	ELYD	APG	WLIW	TYR	TR	TVN	CLIT	OMMAK
CMV	YSRV	IGGT	VFV	AYIIR	DSYEN	KTMOL	IPDD	YSNTH	STR	YVTV	KDOW	HSG	STW	LYR	ETCN	LCML	TTITTAR
HSV	AKYVR	NNLE	TTAF	HRDD	HETD	MELK	-PAN	AART	SRG	WH	TTDL	KYN	PSR	VEA	FHRY	GTTV	NCIVEEVDAR

Fig. 2(c)

EBV	ARGSTPAVLR	RRRRRDAGN	ATT	PP	TAPGKSLG	TLNNPAT	VQIOFAYD	SLRRQINR	MLGDLAR	AWCLEQ
CMV	-----	SDNNT	THLSS	ME	SVH	-----	NLVYAOL	OFTYD	TLRGYIN	RALAQIAE
HSV	-----	ANAS	VERIK	TT	SSIEF	-----	ARLQFT	YNHIO	RHVND	MLGRVAIA
EBV	KRONMVL	RELTKIN	PT	TV	MSS	IYGK	AVAAK	RLGDV	ISV	SOCV
CMV	-----	RRTLEV	FKEL	S	IN	PSAIL	SAIYN	KPIAR	FMGDV	LGLASC
HSV	NHEL	TLWNEAR	KLN	PN	AI	ASAT	VG	RKVSAR	HLGDV	MAVST
EBV	SFS	FIND	TK	TYE	GOLG	TDNEI	FLTK	KMT	EV	CQAT
CMV	-----	IFNFAN	SSYV	OY	GOLG	EDNEI	LLGN	HRT	EE	COL
HSV	SFR	YEDQ	G	PL	VE	GOLG	ENNEL	RL	TR	DAIE
EBV	LNTSL	IENID	FAS	LE	LYS	RDE	QRA	SNV	FD	LF
CMV	-----	LDID	PLE	NT	DFR	VLE	LYS	OKEL	RSS	NV
HSV	LNIT	MLE	D	HE	FV	PLE	VT	TR	HEI	KDS

EBV	DSLGSVGOSITNLVSTVGGLFSSLSVSGFISFFKPNPFEGGMLILVLVAGVVILVISLTLTRRTROMSQQPVMQL
CMV	SGLGAAGKAVGVAIGAVGGAVASVEGVATFLKNPFGAFTIILVAIAVVIITYLIYTRQRRLLCTOPLNCL
HISV	EGMGDLGRAVGKVVMGIVGGVVSAVSGVS\$SFHSPNPF GALAVGLLVLAGLAAAFFAFRYYVMRLQSNNPKMAL

EBV : YPGI-DELAQQH-- --ASGEGPGINPISKTELQ-AIMLALHEQNQEKRAAORAAGPSVASRALOAAARDRF
CMV : FPYLVSADGTTVTSGSTKDTLSLOAPPSYEESVYNSGRKGGCPASSDASTAAPPYTNEQAYOMLLALARLD
HSV : YPLTTKELKNPTNPDASGEGEGGDFDEAKLAEAREMIRYMALVSAMERTEHKAKKKKGTGTS-ALLSAKVTD

ERV PGLRRRRYHDPETAAALLGEA-ETEF
 :
 CMV AEQRAQONGTDSLDGGTGCTQDKGCKPNLLDRLRHRKNGYRHLKDSDEENV
 :
 HSV MVMRKRRRNTNYTQVPNKDGDADDDLL

Fig.3(a)

↓
1 CCGCGCGCTCTCGGGTGTCTTCAGGGAGCGCACCGACCTTGCGTGC'CAAGTCGGTATCCCTCTCTCGACTGCGGGTGTTCGCGAGGGTCCGCGGACACGCCAAGAGACCGAC
121 GCGCGTCACTCGTCTGCGATTTGCGCGGACCGAACATGGAATCCAGGATCTGCGTGCCTGAGTCTGCGTTAACCTGTGTATCGTCTGCTGGGTGCTGCGGTTCTCTTAGTACT
M E S R I W C L V V C V N L C I V C L G A A V S S S T
S H A T S S T H N G S H T S R T T S A Q T R S V Y S Q H V T S S E A V S H R A N
241 TCCATGCAACTCTTCTACTCACAATGGAAGCCATACTCTCGTAGCGGTCTGCTCAAAACCGGTCACTATTCTCAACACGTAACGCTCTCTGAAGCCGTCACTATAGAGCCAAC
E T I Y N T T L K Y G D V V G V N T T K Y P Y R V C S M A Q G T D L I R F E R N
361 GAGACTATCACAACACTACCTCAAGTACGGAGATGTGTGGGAGTCAACACTACCAAGTACCCCTATCGCGTGTCTATGCCCCAGGGTACGGATCTTATTCGCTTTGAAAGTAA
I I C T S M K P I N E D L D E G I M V V Y K R N I V A H T F K V R V Y Q K V L T
481 ATCATGTGCACCTCGATGAAGCCTATCAATGAAGACTTGGATGAGGGCATCATGTGGGTCTACAGCGCAACATCGTGGCGCACACCTTTAAGGTACGGGTCTACCAAAGGTTTTCACG
F R R S Y A Y I Y T T Y L L G S N T E Y V A P P M W E I H H I N K F A O C Y S S
601 TTTCGTGTAGCTAGCTTACATCTACACCACTTATGTGCTGGGAGCAATACGGAAATAGTGGCGCTCTCTATGTGGAGATTTCATCACAATCAACAAGTTTGTCTCAATGTCTACAGTTCC
Y S R V I G G T V F V A Y H R D S Y E N K T M O L I P D D Y S N T H S T R Y V T
721 TACAGCCGCTTATAGGAGGCACGGTTTTCGTGGCATATCATAGGACAGTTATGAACAAACCATGCAATTAAATTCGACGATTATTCACACACCCACAGTATCCGTTACGTGACG
V K D Q W R S R G S T W L Y R E T C N L N C M L T I T T A R S K Y P Y R F F A T
841 GTCAAGGATCAGTGGCACAGCCGCGCAGCACCTGGCTCTATCGTGAGACCTGTATCTGAACCTGTATGCTGACCAATCACTACTGGCGGCTCCAGGTATCTTATCATTTTTTTTGCACCT
S T G D V V Y I S P F Y N G T N R N A S Y F G E N A D K F F I F P N Y T I V S D
961 TCCAGGGTGATGTGTTTACATTTCTCTTCTACAGGGAACCAATCCCAATGCCAGTACTTTGGAGAAACCGCGACAGTTTTTTCATTTTCCGAACTACACCATCGTTTCGAC

Fig.3(b)

F G R P N A A P E T H R L V A F L E R A D S V I S W O J O D E K N V T C O L T F
1081 TTGGAAGACCAACGCTGCGCAGAACCCATAGGTGTGGCTTTCTCGAACGTGCGACTGCGTGAATCTTTGGGATATACAGGACGAGAGAATGTCACTGCCAGCTCACCTTC
W E A S P R T I R S E A E D S Y H F S S A K M T A T F L S K K O E V N M S D S A
1201 TGGGAGCTCGGAACGTACTATCGTTCCGAAGCCGAAGACTCGTACCCTTTCTTGTCCAAATGACTGCAACTTTTCTGCTTAAGAAACAAGTGAACATGTCCGATCTCCGCG
L D C V R D E A I N K L O O I F N T S Y N O T Y E K Y G N V S V F E T S G G I V
1321 CTGGACTCGGTACGTGATGAGGCTATAAATAGTTACAGCAGATTTTCAAJACTTCAACAATCAACATATGAAATAACGGAACGCTGCTCGTCTCGAACCAGCGCGCTGTGGTG
V F W O G . I K Q K S L V E L F E R L A N R S S I . N I T H R T R R S T S D N N T T H
1441 GTGTTCTGGCAAGGCATCAAGCAAAATCTTTGTGGCAATTGGAACGTTTGGCCAATCGATCCAGTCTGAAATACCTCATAGGACCAGAGAAGTACGAGTGACAATAATACAACTCAL
L S S M E S V H N L V Y A O L O F T Y D T L R G Y I N R A L A O J A E A W C V D
1561 TTGTCAGCATGGAAATCGGTGCCAATCTGTGCTACGCCAGCTGCAGTTCACTATGACACGTTGCCGGTTACATCAACCGCGCGCTGGCGCAAAATCGCAGAGCCTGTGGTGTGGAT
Q R R T L P V F K E L S K I N P S A I L S A I Y N K P I A A R F M G D V L G L A
1681 CAACGGCGCACCTAGAGTCTCAAGGAACCTCAGCAAGATCAACCGTCAGCCCAATCTCTCGGCCATTTACACAACCGGATTCGCGCGCTTCATGGGTGATGTCTTGGCTGGCG
S C V T I N Q T S V K V L R D M N V K E S P G R C Y S R P V V I F N F A N S S Y
1801 AGCTGGGTGACCATCAACCAACAGCGTCAAGGTGCTGGCGTGAATGCAAGTGAAGGAATCGCCAGGACGCTGTACTCAGGACCCGTGCTCATCTTTAAATTCGCCAACAGGCTCGTAC
V Q Y G Q L G E D N E I L L G N H R T E E C O L P S L K I F I A G N S A Y E Y V
1921 GTCGAGTACGTCAACTGGCGGAGGACAAAGAAATCTGTGTGGGCAACCAACCGCACTGAGGAATGTCAGCTTCCAGCCTCAAGATCTTCATCGCCGGGAACTCGGCTACGAGTACGTC
D Y L F K R M I D L S S I S T V D S M I A I . D I D P L E N T D F R V L E L Y S O
2041 GACTACCTCTTCAAACGCATGATGACCTCAGCAGTATCTCCACCCTGCAGCAGCATGATCGCCCTGGGATATCGACCGCTGGAAATACCGAACTTCAGGGTACTGGAACTTACTCGCAG

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Fig.4.

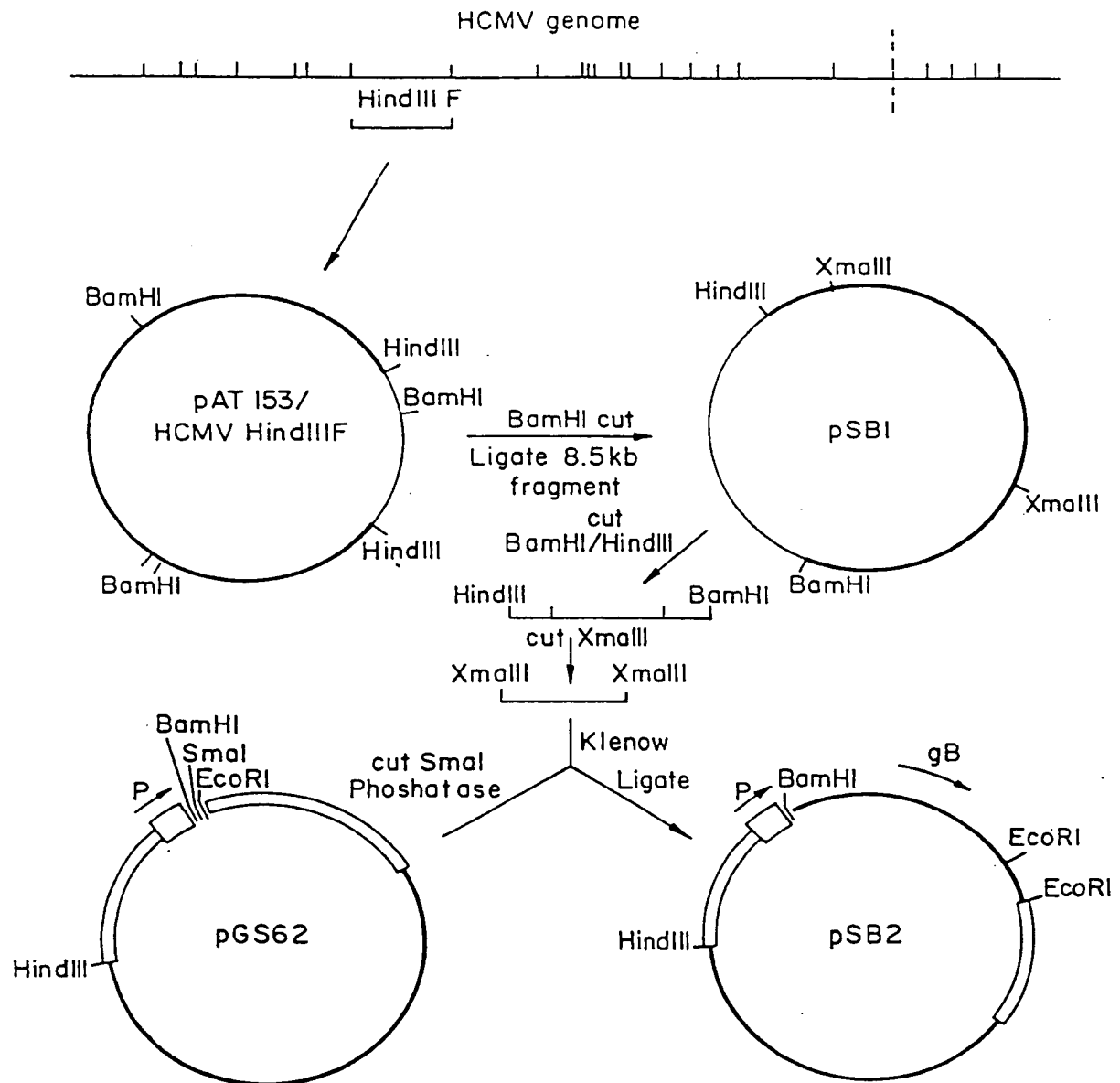


Fig. 5(a)

CGCAGAGCGTTCCCCCGTTCGAATCAGCGTTCGTCCTCCCGACGCCGGCAGGCATGGCTTACCCG

61 CGTGTCCCCTCTTCTTCCTTCGCAGCGGCCAATGACATCGTATTAAATAGACAGAGACGC

121 GACTTTTGTAAACCGTAGCGCCACACCCGGGTGCCCTTCCTGGGATCCTTTCTCTCCTT

181 CTCTCGGGTGTAACGCCAACCACCACCTGGATCAGCGCGCTGAACCCAGCGGGCGCAGCC

M R P G L P P Y L T V F T V Y L L S H

241 CGCTATGCGGCTCCCGGCCTCCCCCCTACCTCACTGTCTTCACCGTCTACCTCCTCAGTCA

L P S Q R Y G A D A A S E A L D P H A F

301 CCTACCTTCGCAACGATATGGCGCGGACGCCGCATCCGAAGCGCTGGACCCTCACGCATT

H L L L N T Y G R P I R F L R E N T T Q

361 TCACCTACTACTCAACACCTACGGGAGACCCCATCCGCTTCCTGCGTGAAAACACCACCCA

C T Y N S S L R N S T V V R E N A I S F

421 GTGCACCTACAACAGCAGCCTCCGTAACAGCACGGTCGTCAGGGAAAACGCCATCAGTTT

N F F Q S Y N Q Y Y V F H M P R C L F A

481 CAACTTTTTTCCAAAGCTATAATCAATACTATGTATTCCATATGCCTCGATGTCTTTTTGC

G P L A E Q F L N Q V D L T E T L E R Y

541 GGGTCCTCTGGCGGAGCAGTTTCTGAACCAGGTAGATCTGACCGAAACCCTAGAAAGATA

Q Q R L N T Y A L V S K D L A S Y R S F

601 CCAACAGAGACTTAACACCTACGCATTGGTATCCAAAGACCTGGCCAGCTACCGATCTTT

S Q Q L K A Q D S L G Q Q P T T V P P P

661 TTCGCAGCAGCTGAAGGCACAAGACAGCCTGGGTGAGCAGCCACCACCGTGCCACCGCC

I D L S I P H V W M P P Q T T P H D W K

721 CATTGATCTGTCAATACCTCACGTTTGGATGCCACCCCAAACCACTCCACACGACTGGAA

G S H T T S G L H R P H F N Q T C I L F

781 GGGATCGCACACCACCTCGGGACTACATCGGCCACACTTTAACCAGACCTGTATCCTCTT

D G H D L L F S T V T P C L H Q G F Y L

841 TGATGGACACGATCTGCTTTTACGACCGTTACGCCCTGTCTGCACCAGGGCTTTTACCT

M D E L R Y V K I T L T E D F F V V T V

901 CATGGACGAACTACGTTACGTTAAATCACACTGACCGAGGACTTCTTCGTAGTTACGGT

S I D D D T P M L L I F G H L P R V L F

961 ATCTATAGACGACGACACACCCATGCTGCTTATCTTCGGTCATCTTCCACGCGTACTCTT

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Fig.5(b)

K A P Y Q R D N F I L R Q T E K H E L L
102| CAAAGCGCCCTATCAACGCGACAACCTTTATACTACGACAACTGAAAAACACGAGCTCCT
V L V K K A Q L N R H S Y L K D S D F L
108| GGTACTAGTTAAGAAAGCTCAACTAAACCGTCACTCCTATCTCAAAGACTCGGACTTTCT
D A A L D F N Y L D L S A L L R N S F H
114| CGACGCCGCACTCGACTTCAACTACCTGGACCTCAGCGCACTGTTACGTAACAGCTTTCA
R Y A V D V L K S G R C Q M L D R R T V
120| CCGTTACGCTGTAGACGTACTCAAAAGCGGTGCGATGTCAAATGTTGGACCGCCGCACGGT
E M A F A Y A L A L F A A A R Q E E A G
126| AGAAATGGCCTTCGCCTACGCATTAGCACTGTTTCGCGGCAGCCCGACAAGAAGAGGCCGG
T E I S I P R A L D R Q A A L L Q I Q E
132| CACCGAAATCTCCATCCCACGAGCCCTAGACCGCCAGGCCGCACTCTTACAAATACAAGA
F M I T C L S Q T P P R T T L L L Y P T
138| ATTTATGATCACCTGCCTCTCACAAACACCACCACGCACCACATTGCTGCTATATCCCAC
A V D L A K R A L W T P D Q I T D I T S
144| AGCCGTGGACCTGGCCAAACGAGCCCTCTGGACGCCGGACCAGATCACCGACATCACCAG
L V R L V Y I L S K Q N Q Q H L I P Q W
150| CCTCGTACGCCTGGTCTACATACTTTCTAAACAGAATCAGCAACATCTCATTCGCCAGTG
A L R Q I A D F A L Q L H K T H L A S F
156| GGCACTACGACAGATCGCCGACTTTGCCCTACAATTACACAAAACGCACCTGGCCTCTTT
L S A F A R Q E L Y L M G S L V H S M L
162| TCTTTCAGCCTTCGCGCGCCAAGAACTCTACCTCATGGGCAGCCTCGTCCACTCCATGTT
V H T T E R R E I F I V E T G L C S L A
168| GGTACATACGACGGAGAGACGCGAAATCTTCATCGTAGAAACGGGCCTCTGTTTCATTGGC
E L S H F T Q L L A H P H H E Y L S D L
174| CGAGCTATCACACTTTACGCAGTTGCTAGCTCATCCGACCACGAATACCTCAGCGACCT
Y T P C S S S G R R D H S L E R L T R L
180| GTACACACCCTGTTCCAGTAGCGGGCGACGCGATCACTCGCTCGAACGCCTCACGCGTCT
F P D A T V P A T V P A A L S I L S T M
186| CTTCCCGATGCCACCGTTCCCTGCTACCGTTCCCGCCGCCCTCTCCATCCTATCTACCAT
Q P S T L E T F P D L F C L P L G E S F
192| GCAACCAAGCACGCTGGAAACCTTCCCCGACCTGTTTGTCTGCCGCTCGGCGAATCCTT

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Fig.5(c)

S A L T V S E H V S Y V V T N Q Y L I K
198| CTCCGCGCTAACCGTCTCCGAACACGTCAGTTATGTCGTAACAAACCAGTACCTGATCAA
G I S Y P V S T T V V G Q S L I I T Q T
204| AGGTATCTCCTACCCTGTCTCCACCACCGTCGTAGGCCAGAGCCTCATCATCACCCAAAC
D S Q T K C E L T R N M H T T H S I T A
210| GGACAGTCAAACATAAATGCGAACTAACGCGCAACATGCACACCACACACAGCATCACAGC
A L N I S L E N C A F C Q S A L L E Y D
216| GGCGCTCAACATTTCACTAGAAAACGCGCCTTTTGCCAAAGCGCCCTGCTAGAATACGA
D T Q G V I N I M Y M H D S D D V L F A
222| CGACACGCAAGGCGTCATCAACATCATGTACATGCACGACTCGGACGACGTCCTTTTCGC
L D P Y N E V V V S S P R T H Y L M L L
228| CCTGGATCCCTACAACGAAGTGGTGGTCTCATCTCCGCGAACTCACTACCTCATGCTTTT
K N G T V L E V T D V V V D A T D S R L
234| GAAAAACGGTACGGTCCTAGAAGTAACTGACGTCGTCGTGGACGCCACCGACAGTCGTCT
L M M S V Y A L S A I I G I Y L L Y R M
240| CCTCATGATGTCCGTCTACGCGCTATCGGCCATCATCGGCATCTATCTGCTCTACCGCAT
L K T C
246| GCTCAAGACATGCTGACTGTAGAACCTGACAGTTTATGAGAAAAGGGACAGAAAAGTTAA
252| AGACATTACACAAAATCTTCTAAAACGGTACGGGGCCCCAATACTTAGGGGCACTCTTGC
258| TCGTTGTAATAAAGTACACGCCACACGGTGTGATGGTACTATATGCGTGAGGTCTGTGCG
264| TCTTTATTTACGAGGTACTGTTATGGGTCTGGTTACATATCGGGCCCTGGATACAAGCTT
HindIII